

Fig. 1

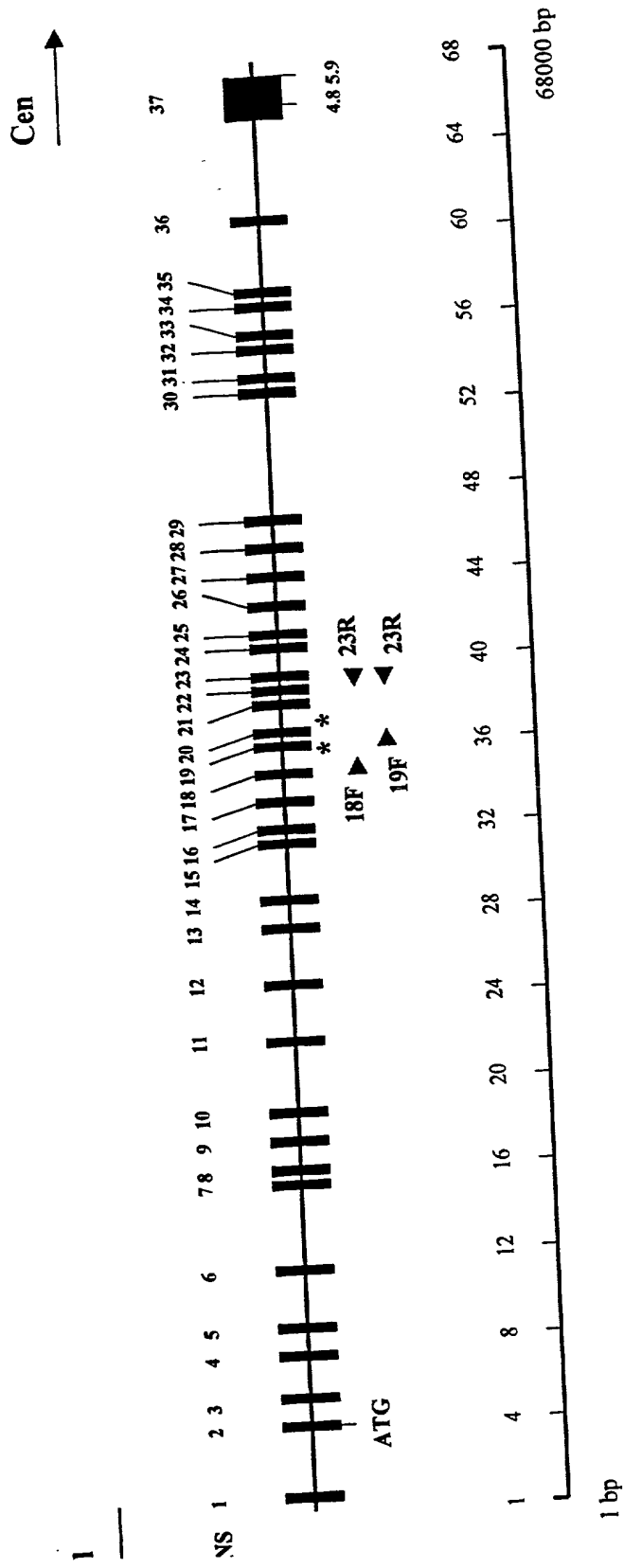


Fig. 2a

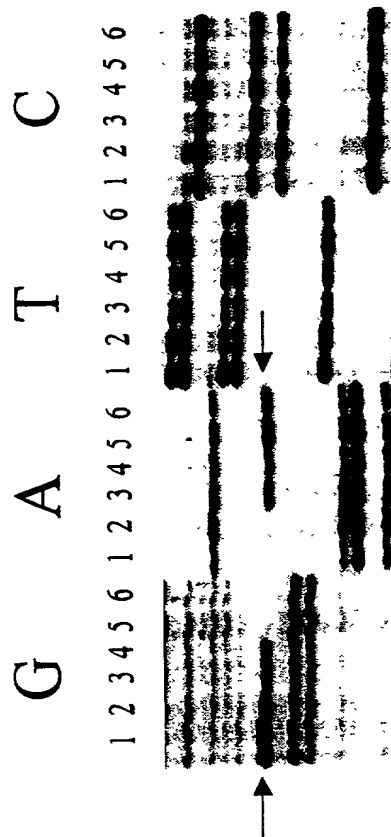


Fig. 2c

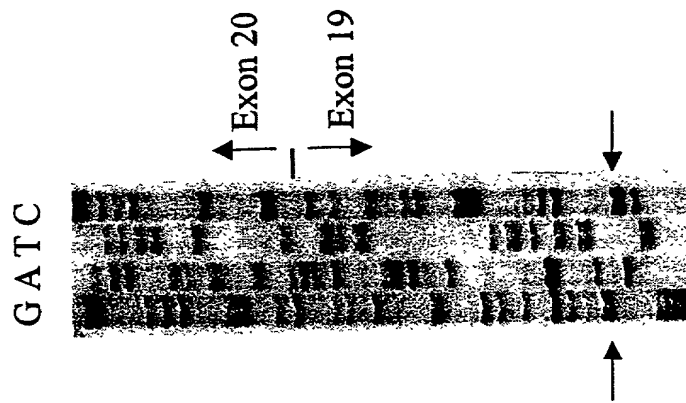


Fig. 2b

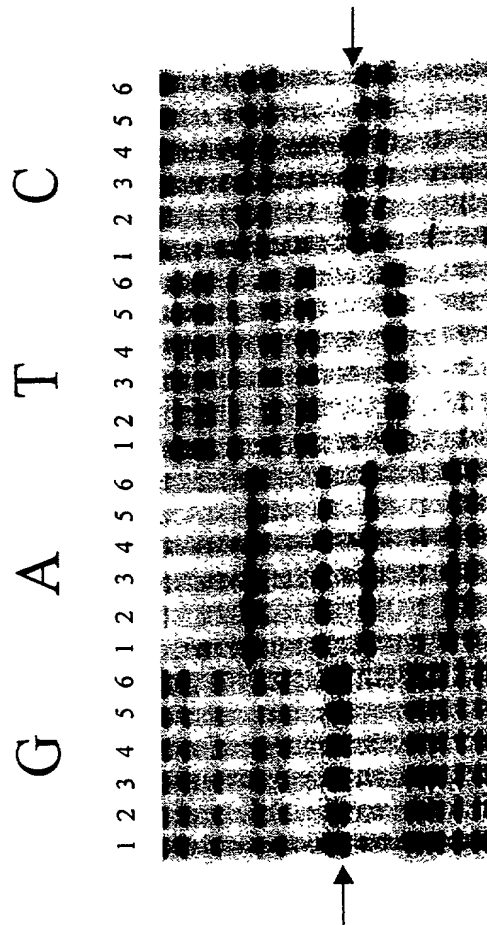


Fig. 3A

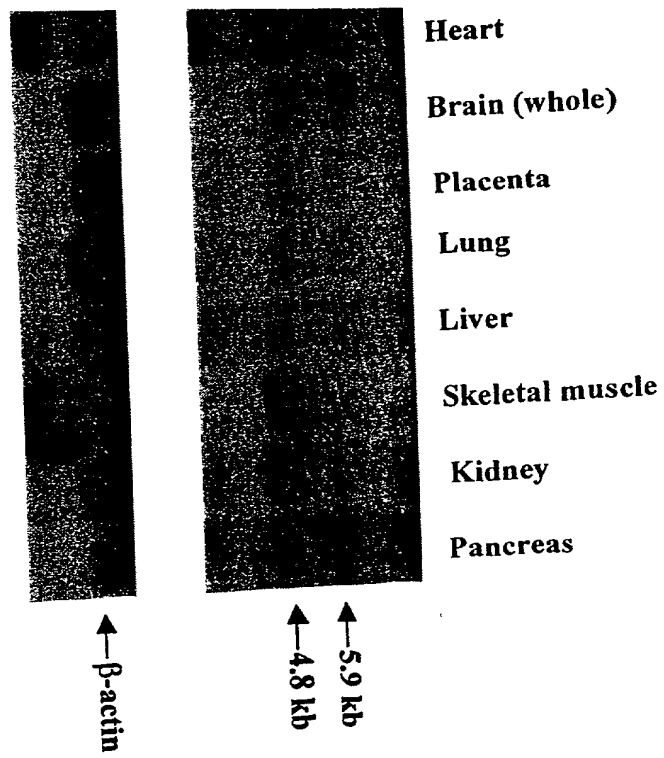
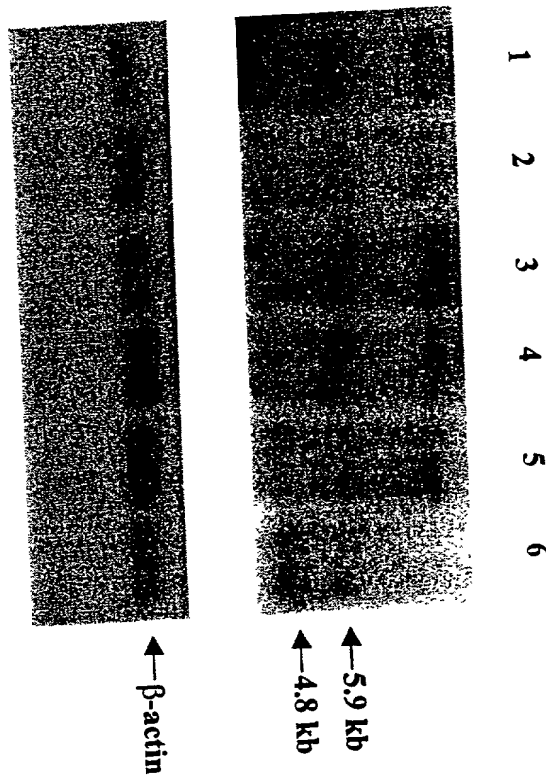


Fig. 3B



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FIG. 4A

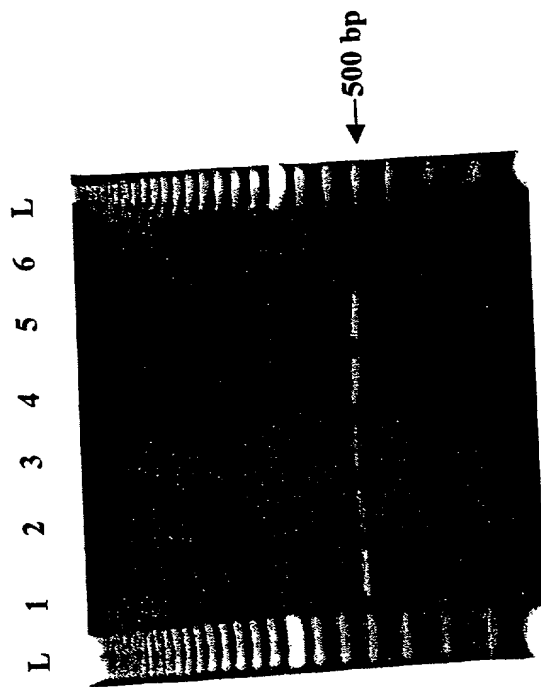
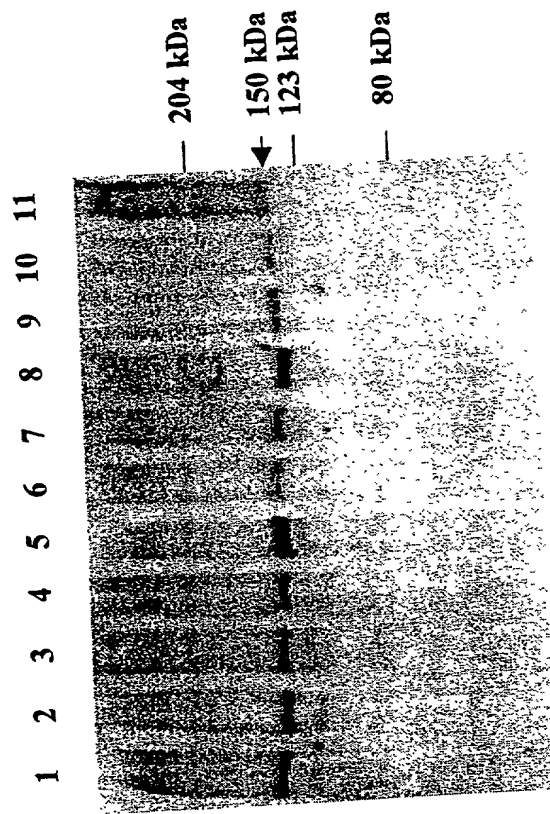


FIG. 4B



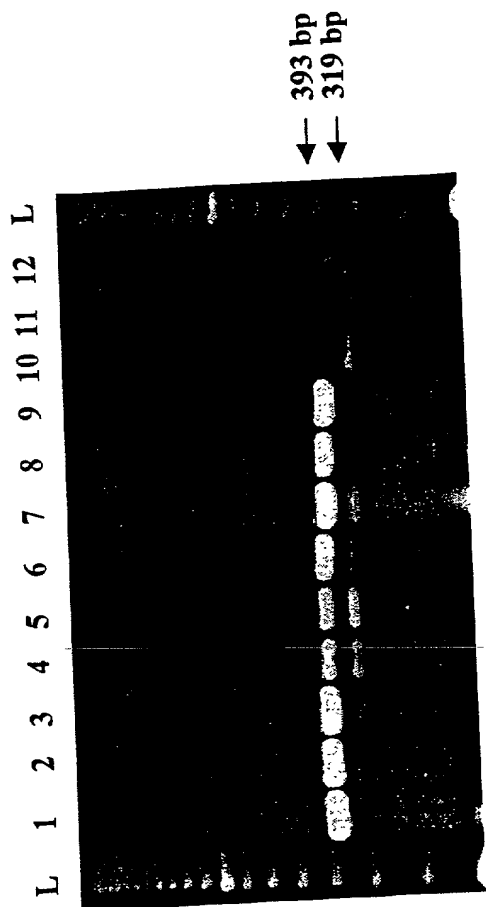


FIG. 5

## FIGURE 6

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66301 TTACATGGGT TTGCTGTAAT TAAGTGCCCA ATATTGAAAG GCTGCAAGTA  
66351 CTTTGTAATC ACTCTTTGGC ATGGGTAAAT AAGCATGGTA ACTTATATTG  
66401 AAATATAGTG CTCTTGCTTT GGATAACTGT AAAGGGACCC ATGCTGATAG  
66451 ACTGGAAATA GAAGTAAATG TGTTTATTG

FIGURE 7

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1 ccagtgcctgg ggctgcctag ttgacgcacc cattgagtcg ctggcttctt tgcagcgctt
61 cagcggttttc ccctggaggg cgcctccatc cttggaggcc tagtgccgtc ggagagagag
121 cgggagccgc ggacagagac gcgtgcgcaa ttcggagccg actctgggtg cggactgtgg
181 gagctgactc tgggtagccg gctgcgcgtg gctggggagg cgaggccgga cgcacctctg
241 tttgggggtc ctcagagatt aatgattcat caagggatag ttgtactgtt ctctgtggaa
301 tcacttcatc atgcgaaatc tgaattatt tccgaccctg gagttcaggg atattcaagg
361 tccagggaat cctcagtgtc tctctctccg aactgaacag gggacggtgc tcattgggtc
421 agaacatggc ctgatagaag tagaccctgt ctcaagagaa gtgaaaaatg aagtttcttt
481 ggtggcagaa ggctttctcc cagaggatgg aagtggccgc attgttgggtg ttcaggactt
541 gctggatcag gagtctgtgt gtgtggccac agcctctgga gacgtcatatc tctgcagtct
601 cagcacacaa cagctggagt gtgttgggag tgtagccagt ggtatctctg ttatgagttg
661 gagtctgac caagagctgg tgcttcttgc cacaggtcaa cagaccctga ttatgatgac
721 aaaagatttt gagccaatcc tggagcagca gatccatcag gatgattttg gtgaaagcaa
781 gtttatcact gttggatggg gtaggaaagg gacacagttc catggatcag aaggcagaca
841 agcagctttt cagatgcaaa tgcattgagtc tgctttgccc tgggatgacc atagaccaca
901 agttacctgg cggggggatg gacagttttt tgctgtgagt gttgtttgcc cagaaacagg
961 ggctcggaag gtcagagtgt ggaaccgaga gtttgctttg cagtcaacca gtgagcctgt
1021 ggcaggactg ggaccagccc tggcttgaaa accctcaggc agtttgattg catctacaca
1081 agataaacc aaccagcagg atattgtgtt ttttgagaaa aatggactcc ttcattggaca
1141 ctttacactt cccttcctta aagatgaggt taaggtaaat gacttgctct ggaatgcaga
1201 ttcctctgtg cttgcagtct ggctggaaga ccttcagaga gaagaaagct ccattccgaa
1261 aacctgtgtt cagctctgga ctgttggaat ctatcactgg tatctcaagc aaagtttatc
1321 cttcagcacc tgtgggaaga gcaagattgt gtctctgatg tgggaccctg tgacccata
1381 ccggctgcat gttctctgtc agggctggca ttacctcgcc tatgattggc actggacgac
1441 tgaccggagc gtgggagata attcaagtga cttgtccaat gtggctgtca ttgatggaaa
1501 cagggtgttg gtgacagtct tccggcagac tgtggttccg cctcccatgt gcacctacca
1561 actgctgttc ccacaccctg tgaatcaagt cacattctta gcacaccctc aaaagagtaa
1621 tgaccttgct gttctagatg ccagtaacca gatttctgtt tataaatgtg gtgattgtcc
1681 aagtgtgac cctacagtga aactgggagc tgtgggtgga agtggattta aagtttgctt
1741 tagaactcct catttggaat agagatacaa aatccagttt gagaataatg aagatcaaga
1801 tgtaaaccgg ctgaaactag gccttctcac ttggattgaa gaagacgtct tctgtgctgt
1861 aagccacagt gagttcagcc cccggtctgt cattcccat ttgactgcag cttcttctga
1921 gatggatgaa gagcatggac agctcaatgt cagttcatct gcagcgggtg atggggtcat
1981 aatcagtcct tgttgcaatt ccaagaccaa gtcagtagta ttacagctgg ctgatggcca
2041 gatattttaag tacctttggg agtcaccttc tctggctatt aaacctatga agaactctgg
2101 tggatttctt gttcgggttc cttatccatg caccagacc gaattggcca tgattggaga
2161 agaggaatgt gtccttggtc tgactgacag gtgtcgcttt tcatcaatg acattgaggt
2221 tgcgtcaaat atcacgtcat ttgcagtata tgatgagttt ttattgttga caaccattc
2281 ccataacctg cagtgttttt gcctgaggga tgcttcattt aaaacattac aggcgggctt
2341 gagcagcaat catgtgtccc atggggaagt tctgcgaaa gtggagaggg gttcacggat
2401 tgtcactgtt gtgccccagg acacaaagct tgtattacag atgccaagg gaaacttaga
2461 agttgttcat catcgagccc tggttttagc tcagattcgg aagtgggttg acaaacttat
2521 gtttaaagag gcatttgaat gcatgagaaa gctgagaatc aatctcaatc tgatttatga
2581 tcataacctt aaggtgtttt ttggaaatgt ggaaaccttc attaaacaga tagattctgt
2641 gaatcatatt aacttgtttt ttacagaatt gaaagaagaa gatgtcacga agaccatgta
2701 ccctgcacca gttaccagca gtgtctacct gtccagggat cctgacggga ataaaataga
2761 ccttgtctgc gatgctatga gagcagtcac ggagagcata aatcctcata aatactgctt
2821 atccatactt acatctcatg taaagaagac aaccccagaa ctggaaattg tactgcaaaa
2881 agtacacgag cttcaaggaa atgctccctc tgatcctgat gctgtgagtg ctgaagaggc
2941 cttgaaatat ttgctgcac tggtagatgt taatgaatta tatgatcatt ctttggcac
3001 ctatgacttt gatttggctc tcatggtagc tgagaagtca cagaaggatc ccaaagaata
3061 tcttccattt ctaatacac ttaagaaaat ggaaactaat tatcagcggg ttactataga
3121 caaatacttg aaacgatatg aaaaagccat tggccacctc agcaaagtgt gacctgagta

```

Figure 7  
Continued

3181	cttcccagaa	tgcttaaact	tgataaaaga	taaaaacttg	tataacgaag	ctctgaagtt
3241	atattcacca	agctcacaa	agtaccagga	tatcagcatt	gcttatggg	agcacctgat
3301	gcaggagcac	atgtatgagc	cagcggggct	catgtttgcc	cgttgcgggtg	cccacgagaa
3361	agctctctca	gcctttctca	catgtggcaa	ctggaagcaa	gccctctgtg	tggcagccca
3421	gcttaacttt	accaaagacc	agctgggtgg	cctcggcaga	actctggcag	gaaagctggt
3481	tgagcagagg	aagcacattg	atgcggccat	ggttttggaa	gagagtgcc	aggattatga
3541	agaagctgtg	ctcttgctgt	tagaaggagc	tgccctgggaa	gaagctttga	ggctggtata
3601	caaatataac	agactggata	ttatagaaac	caacgtaaag	ccttccattt	tagaagccca
3661	gaaaaattat	atggcatttc	tggactctca	gacagccaca	ttcagtcgcc	acaagaaacg
3721	tttattggta	gttcgagagc	tcaaggagca	agcccagcag	gcaggtctgg	atgatgaggt
3781	accccacggg	caagagtcag	acctcttctc	tgaaaactagc	agtgtcgtga	gtggcagtga
3841	gatgagtggc	aaatactccc	atagtaactc	caggatatca	gcgagatcat	ccaagaatcg
3901	ccgaaaagcg	gagcgggaaga	agcacagcct	caaagaaggc	agtcgcgtgg	aggacctggc
3961	cctcctggag	gcactgagtg	aagtgggtgca	gaacactgaa	aacctgaaag	atgaagtata
4021	ccataatttta	aaggtactct	ttctctttga	gtttgatgaa	caaggaagg	aattacagaa
4081	ggcctttgaa	gatacgctgc	agttgatgga	aaggtcactt	ccagaaattt	ggactcttac
4141	ttaccagcag	aattcagcta	ccccggttct	aggtcccaat	tctactgcaa	atagtatcat
4201	ggcatcttat	cagcaacaga	agacttcggt	tcctgttctt	gatgctgagc	ttttataacc
4261	accaaagatc	aacagaagaa	cccagtgga	gctgagcctg	ctagactgag	tgactgcagt
4321	taggagggat	ccgacagaga	agaccatttc	cactcattcc	tgttgtccta	ccaccccttg
4381	ctctttgagg	gctggctatt	gagaactgga	aagagtaaaa	tgataactta	ccttagcatt
4441	gccaaagaact	tcagcagaca	acaagcaatt	ctatttat	tatgttgtgt	atacatcttg
4501	atcattagca	agacattaag	ctttaaccat	tatggcacca	ttttgtgaga	atgattgttc
4561	tttactctgg	gctgtttgag	agcataatta	tggtaatcat	gagattaatg	tttcatgatt
4621	tctacctcca	aagtgtgaag	acaagtaaaa	caatgtttct	aaattgtctt	attttgttgg
4681	cggagaagat	tacaatggct	attagtgtca	catttgggtca	aatgtaatca	cttaaatagc
4741	ttcttgtcac	cttaaaactaa	agcagaataa	aaagtatcct	ttgaaattat	aagccctcct
4801	ttgctgacag	ctattatttt	gtaacatctt	accaggtoat	gtgctttcag	ttataactgg
4861	gctgagcctc	ctataattac	aatgtctata	gggactgttt	tactgcctgt	gtattttctg
4921	ctagagagtt	agcaatgtta	gagctagaac	agattagaat	ttctaaacag	tatcatgcac
4981	agttgggtgtg	agtgtacagt	gtgcattgta	tggcatgcat	ggttgtgaat	tattctctgt
5041	tctccaaata	ctgtttcttt	aactcagata	tttttgtag	tgtctaggcc	acttcattta
5101	tttttcgtca	tggtacttta	ctgacttctc	tttattcaat	tctocacgcc	ctcaccaaaa
5161	aaaactgtct	caaaatgaga	atatttttat	tcttcatggt	gagtctagaa	aacgccccac
5221	ttcattctga	ttaaaaaatt	cttccatgtt	tttaaatatc	agaaccagac	ctttcttact
5281	gtgtatctta	gccattttgt	gtctctataa	caacaaccag	ctttcaaagg	aactaataga
5341	gtgaaaactc	actcattacc	acgaggatgg	cacaagcgat	tcacgtagga	tctgcccctg
5401	tgacaaaaac	acctcccatt	gggccccact	tccaacactg	gtgatcacat	ttcaacatga
5461	ggtttaggga	aacaaatgcc	taaactacag	cactgtacat	aaactaacag	gaaatgctgc
5521	ttttgatcct	caaagaagtg	atatagccaa	aattgtaatt	taagaagcct	ttgtcagtat
5581	agcaagatgt	taactataga	atcaatctag	gagtattcac	tgtaaaattc	aacttttctg
5641	tatgtttgaa	cattttcaca	atctcatagg	agtttttaaa	aagaagagaa	agaagatata
5701	ctttgctttg	gagaaatcta	ctttttgact	tacatgggtt	tgctgtaatt	aagtgcccaa
5761	tattgaaagg	ctgcaagtac	tttgtaatca	ctctttggca	tgggtaaata	agcatggtaa
5821	cttatattga	aatatagtgc	tcttgctttg	gataactgta	aagggaccca	tgctgataga
5881	ctggaaatag	aagtaaatgt	gtttattgaa	aaaaaaaaa	aaaa	

4041356.010702

# FIGURE 8

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1 mrnlklfrtl efrdiqgpgn pqcfslrteq gtvligsehq lievdpsvre vknevsivae
61 gflpedgsgv ivgvqdllldq esvcvatasg dvlcslstq qlecvgsvas gisvmswspd
121 qelvllatgq qtlimtkdf epileqqihq ddfgeskfit vgwgrketqf hgsegrqaaf
181 qmqmhesalp wddhrpqvtw rgdgqffavs vvcpetgark vrvwnrefal qstsepvagl
241 gpalawkpsg sliastqdkp nqqdivffek ngllhghftl pflkdevkvn dllwnadssv
301 lavrledlqr ekssipktcv qlwtvgnyhw ylkqslsfst cgkskivslm wdpvtpyrlh
361 vlcqgwhyla ydwhwttdrs vgdnsdlsn vavidgnrvl vtvfrqtvvp ppmctyqllf
421 phpvnqvtfll ahpqksndla vldasnqisv ykcgdcpsad ptvklgavvg sgfkvcrltp
481 hlekrykiqf ennedqdvnp lklglwtwie edvflavshs efsprsvihh ltaassemde
541 ehgqlnvsss aavdgiisll ccnsktksvv lqladgqifk ylwespslai kpwknsaggfp
601 vrfpypctqt elamigeeec vlgltdrcrf findievasn itsfavydef llltthshtc
661 qcfcldrdsf ktlqaglssn hvshgevlrk vergsrivtv vpgdtklvlg mprgnlevvh
721 hralvlaqir kwldklmfke afecmrklri nlnpiydhnp kvflgnvetf ikqidsvnhi
781 nlfftelkee dvtktmypap vtssvylsrd pdgnkidlvc damravmesi nphkyclsil
841 tshvkkttppe leivlqkvhe lqgnapsdpd avsaealky llhlvdvnel ydhslytydf
901 dlvlmvaeks qkdpkeylpf lntlkmetn yqrftidkyl kryekaighl skcgpeyfpe
961 clnlikdnl ynealklysp ssqqyqdisi aygehlmqeh myepaglmfa rcgahekals
1021 afltcgnwkq alcvaqlnf tkdqlvglgr tlagklveqr khidaamvle esaqdyeeav
1081 llllegaawe ealrlvykyn rldietnvk psileaqkny mafldsqtat fsrhkkrllv
1141 vrelkeqaqq aglddevphg qesdlfsets svvsgsemsg kyshsnsris arssknrrka
1201 erkkhslkeg splledlalle alsevvqnte nlkdevyhl kvlflfefde qgrelqkafe
1261 dtlqlmersl peiwtltyqq nsatpvlgnp stansimasy qqktsvpvl daelfippki
1321 nrqtqwklsd ld

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10041335.040702

M_musculus	1	.....MRNLKLETFEFDIOAPCKP.....OCFCLEAE..OGTVLIG
H_sapiens	1	.....MRNLKLETFEFDIOAPCKP.....OCFCLEAE..OGTVLIG
D_melanogaster	1	.....MRNLKLETFEFDIOAPCKP.....OCFCLEAE..OGTVLIG
S_cerevisiae	1	MVEHDKSGSKRQELRSNMRNLITLNKGNKPTAETAGDEDDSTFTLIDVFTLDSIT
A_thaliana	1	.....MRNLKLETFEFDIOAPCKP.....OCFCLEAE..OGTVLIG
C_elegans	1	.....MKNLQIGSKTETENPEIAGADDF..H
M_musculus	37	SERGLTEVDP..VRREVKEHSLVAEGFLPEDGSGCIVGHDLLDQESVOCVATASGDVIV
H_sapiens	37	SEHGLTEVDP..VSREVKNESLVAEGFLPEDGSGCIVGHDLLDQESVOCVATASGDVIV
D_melanogaster	36	FVADNKEVYA..VOESGDVRLKKTAD..LPS.....IVGVGFLDLDNREOVAKKAGVIV
S_cerevisiae	61	CVLGSNLTGATEVQOFNRGGRNVLASNIOTFDKESFVFADINOGVFVFEQGDIT
A_thaliana	43	FVYALQLSSFQNESAGAKSAMPTEVCSDIEPGD.FITFTD.LAEKESHLGTHGLAV
C_elegans	27	PLQTIAVSCKNELLLLENNISSTIKWAEQRRELEVSTSRADGNQEVVILADGRAE
M_musculus	95	C.....NLSTOOLECVGSVASCISVMSWSPDOELLATGOTLIMMTKDFEVLAEQ
H_sapiens	95	C.....NLSTOOLECVGSVASCISVMSWSPDOELLATGOTLIMMTKDFEVLAEQ
D_melanogaster	87	V.....EPONGATSEGTFCVGCIESMAWSPDQERMAFVIRTHNNAETSTFVLAEQ
S_cerevisiae	121	ATYDPLSLPPTETLIEITNGCIAAOWSYDETTLAVTKDRNVAISKLFEPISEYH
A_thaliana	102	.....HNVEFDVTEVCNIGCGKCKSPNPTGELLGITGLGLITNTYDWMYKSA
C_elegans	87	VEDGEVMD.....LELAELTDTYSAAEWMADETLALADN..QTLVHADSSLVFAER
M_musculus	148	T..HODDFEGEGKFTVVGWGSKTOFHGSEGRPTAFEV.....CPENALPDDH
H_sapiens	148	T..HODDFEGEGKFTVVGWGSKTOFHGSEGRPTAFEV.....CPENALPDDH
D_melanogaster	140	M..DAELDPDQCFVNVGCKKKEQFHGSEGRPTAFEV.....CPENALPDDH
S_cerevisiae	181	L..EVDDLKISKFTVVGWGSKTOFHGSEGRPTAFEV.....CPENALPDDH
A_thaliana	155	C...GEVPEGGV.....RET.....
C_elegans	140	IFSENERKSADPVNVGWSSESQFHGSGACKLPGKIEKEK.....
M_musculus	195	R.....PH...LWRGDGGEFAVSVV.....CHOTEARKIRVWRE.FALOSTS
H_sapiens	195	R.....PH...LWRGDGGEFAVSVV.....CHOTEARKIRVWRE.FALOSTS
D_melanogaster	187	L.....PO...LWRGDGGEFAVSVV.....CHOTEARKIRVWRE.FALOSTS
S_cerevisiae	240	TGCVTADSHSHEISISWRGDGEFAVSVVVEVPEDDETMSIKRAFRVFSRE.GOLDSIS
A_thaliana	168	..NDSEVCCGGISISWRGDGKYPAT..MGEVYSGCM.....EKKIKESGALCSIS
C_elegans	181	..KOTEQHSKTSVHRWWDGEIVAVSF.....YSSONDENETVFDNGEITNNMN
M_musculus	235	SVPEGLGALANKPSSGLIATODK.....PNOODVFFFEKNGLLHGHTLPLFLKDEVK
H_sapiens	235	SVVAGLGLALANKPSSGLIATODK.....PNOODVFFFEKNGLLHGHTLPLFLKDEVK
D_melanogaster	229	SKSANLKDSEVNVNPGNWIAPVQOF.....PNKSTIALFEKNGLRHRELVLPPDLOEP
S_cerevisiae	299	EPVNGHEHOLNKPQGLIASIQRTDLGEZSVDMFFPERNGRHRGEDTRLPLDE.M
A_thaliana	219	ETKEFTGILENMPSGATIAAYYKK..SDSSPSIAFEERNGLERSSREGEPEOATES
C_elegans	230	IRNIYVSHCFAPKPNANLECSITQENGSDD....RIVIMEENGETRNSVYKWAANGEZ
M_musculus	289	..VNDLLWNADSSVLAWLEDLPKEDSSTLKSIVOLTVGNYHWYKQSLFSTNGKNQ
H_sapiens	289	..VNDLLWNADSSVLAWLEDLPKEDSSTLKSIVOLTVGNYHWYKQSLFSTNGKNQ
D_melanogaster	283	..VVOLRWSEDSDELAL..RTCAKEQR.....VLYTNGNYHWYKQSLVLIPEDE.DP
S_cerevisiae	357	..VESNCNSNSSEALAM.....VLANRIQLWTSKNYHWYKQSL.....YAD
A_thaliana	277	..CENMKNSADILA.GYVSCCTYDA.....TRNGFFSNHWYKQSLFSTNGKNQ
C_elegans	286	RRIIIEKEWNSGTGELFN.....QTLGKKHQEFPHHSNVEFTRKYWKFSE.....
M_musculus	346	IVSLHWDE..VTECRHLVLCGHWRYLCCDHHWTDRSSCNSANDLANVAVIDGNRVLTU
H_sapiens	346	IVSLHWDE..VTECRHLVLCGHWRYLCCDHHWTDRSSCNSANDLANVAVIDGNRVLTU
D_melanogaster	331	IALLHWDPTRCGKEHTLHVLEKESGKHLVMAFAVDNRRN.....SIVEVIDGKRLTDT
S_cerevisiae	398	TSYKWBEE..KDETLMFSDAGFINIV..DFAYKMAQGPTLPPFENGTSIVDDGRTNNEP
A_thaliana	325	..VTVWDE..TKLQELICNTLSCQVSVRHFMVV.....AVMEDSTAFVIDNSRELVT
C_elegans	334	..STKRWSTVECCNTEVILLESQEFFSVH...IQPTASFSDVLSQNVVATD..LRRNYS
M_musculus	404	FRQTVVPPPMCTYRLILPHPVNOVIFS...AH..LGNDLAVLDASNOISVYKCG..DKPN
H_sapiens	404	FRQTVVPPPMCTYRLILPHPVNOVIFS...AH..LGNDLAVLDASNOISVYKCG..DKPN
D_melanogaster	384	SPDZVPPPMCKE...LQKSE...MLMPDA..EESGLHLA..ALTH
S_cerevisiae	455	LALNVPPPMYIRDFFETEGNVLDVACSFSEIYAAINKDMLFAVPSHEEMKKG..KHPD
A_thaliana	376	LSLNVPPPMYLSLSSESAVRDHAAYSRNS.....KNCLAVFLDGNESFV....KTPA
C_elegans	387	LCRRNVPPPMCDYSIQCLSDI...VAKTSTHVVHVTSSDWKTESCMLFFKKKRNYSNPF
M_musculus	457	MDSTVKLGAVGGNGFKVPLATPHLEKRYSTQFGNNEKEEEDFALQLSFTLWVEEDTFLA
H_sapiens	459	ADPTVKLGAVGGNGFKVPLATPHLEKRYSTQFGNNEKEEEDFALQLSFTLWVEEDTFLA
D_melanogaster	420	ESHYLLATSSAG.....STRLLISMA...DNINKPGD.....H.....FYR
S_cerevisiae	514	IVCE.....EPKSEFTSEVSLRQAFINDSIVGVLLDNDNUSKALNDIQDI..
A_thaliana	427	PNTWEDLEGKDFEVEISDCKALGSEFVHLHLVHSLLCUSAYGSSHNK..CLSSGGYDTE
C_elegans	445	PRKKYIEILKVPSSRTYFACFAYSQDQGYKFNDRASIDEV.....PHTEVTEGICG

FIG. 1. Comparison of the amino acid sequence of Ikap across several species. Alignment of the amino acid sequence of Ikap (M\_musculus) with that of *Homo sapiens* (H\_sapiens), *Drosophila melanogaster* (D\_melanogaster), *Saccharomyces cerevisiae* (S\_cerevisiae), *Arabidopsis thaliana* (A\_thaliana), and *Caenorhabditis elegans* (C\_elegans). Black boxes indicate identical AA, while conserved AA residues are shown in gray. Asterisk (\*) at AA position 696 for mouse and human proteins indicates the location of the heterozygous R696P mutation found in only 4 FD patients. Sequence alignments were made using Pileup and Boxshade commands from GCG Wisconsin Package V.9.0 (Madison, WI).

Figure 9

M_musculus	517	SYSHSSSQSIHHLTVHSEVDEEGQLVSSSVTVDGVVIGLCCC.SKTKSLAVOLAD
H_sapiens	517	VSHSEFSPRSVIHHLTAASSEMDEEHGQLVSSSVTVDGVIISLCCN.SKTKSEVQLAD
D_melanogaster	456	V.HSSRLNGEYNAVAHYAIFYVO.TVNNGHY...SL...KADKRLVERSY
S_cerevisiae	562	TOPALALIVEYDSEVLRSDFDYHLVYE...RDGTVCOLD...A
A_thaliana	486	EHGSYHCEVEVYCHEDHVEDVTCSGFKASITFQKLHESPVALAWNPSKRDSATVFEFEG
C_elegans	500	FVYDEPSESYSILWNVSHKHHS...REGANPEKIFEGENIGWIGVNPSPNKHHEBASND
M_musculus	576	GOVLKILWCSPLSLAEPWKNSEGLVRFVHPCTOMEVANIGGEECVLGLTDRCRFFILVT
H_sapiens	576	GOVFKYLWCSPLSLAEPWKNSGCFVRFVHPCTOTEBAMIGEECVLGLTDRCRFFIND
D_melanogaster	507	VQK...HEPDQDID.VIVVKG...CIWD...GYTGAAZLRVCHLHLEGY
S_cerevisiae	604	GOVNETTKEPDQVVRDFVVKR...VENTSAEDDDNWSKESSELVAFGTNNGLEFANQV
A_thaliana	546	CKVLGYASRSEIMETRSDSEVCFSTCEWVRVAQVDHSGVHKPLCCGIDDMGRSLINGK
C_elegans	556	GKFFEDNTKEELFKIDKFESDEVHFEQVCHGILNHHVTO...DNSMLFSESE
M_musculus	636	EVASNITSFA.....VCDFFLLTTHSH...TCQCESLSGASLKMLOAALSSEHEA
H_sapiens	636	EVASNITSFA.....VDEFLLLTTHSH...TCQCECLRDASFKLOAGLSSNHVS
D_melanogaster	548	RKCEDYTSFC.....VITLHYTO.....LNAMEFVLD...DRROVA
S_cerevisiae	659	LTASAMTSL.....ETSLDFLTAAQH...NLQFVHLNSDDEKPLVLEG...V
A_thaliana	606	NLCNCSSESYSELANEVVTHLELTKQDFFLFIOTKDVNLNGDVILGNFFVVDGGRD
C_elegans	606	RVSODAISILTRG.....SDILLDFDNKLRFDAX.....S
M_musculus	684	SGE...RKVWVGSRIVTVV.PODKRILOMPRGNLEVHHRALVLAQIRKWLDKLMFKE
H_sapiens	684	HGEV...RKVERGSRIVTVV.PODKRILOMPRGNLEVHHRALVLAQIRKWLDKLMFKE
D_melanogaster	584	S...RNPERGSRIVTAV.ARKARVLOMPRGNLEICERVLVLELIGDILG...OK
S_cerevisiae	704	EDER...VRABERGSRIVSVI.BSKESVLOATRGNLETTVPRIIVLAKKNMAKRKE
A_thaliana	666	EENMSYVNIWERGSGVIGVGDAAVILQTMRCNLECTYPRKLVLSITNAQAQRFKE
C_elegans	638	GKTJEDVRNVEACCEGV.ACISGSANVILQAARGNLETTQRRYVFAHTDLDLKEKEA
M_musculus	741	AFECMRKLRINLNLIHD.HNPKVFLENVETFEVFOIDSUNHINLFFTELSEEDVTKTMYPE
H_sapiens	741	AFECMRKLRINLNLIYD.HNPKVFELGNVETFEKOIDSVNHINLFFTELKEEDVTKTMYPA
D_melanogaster	637	ATEMSRKORINLNLIHD.HVVKRFVSSVGNFINDINEPWTCLFLSELONEDFTKGMVSS
S_cerevisiae	761	AEIVCRTHRINLNLIHD.YAPENFENEEVEHINOIGRVVYANLFIISCLSEEDVTKTMYKE
A_thaliana	726	AENLVRHRIDFTNVLIVOLYGOAELQSAVASVEOVNNENHVTSEVCAMKEEDVTETMYKK
C_elegans	797	SEKWMKKHRHMS.....BAMKYKGDDDEDD...B
M_musculus	800	.....PITK.SVOMST...HPDGKKHDLCDAMRAAM..EAINPKEKCLS
H_sapiens	800	.....PYTS.SVYSES...DPDGNKIDLVCDAMRAVM..EAINPKEKCLS
D_melanogaster	696	NY.....DASK.PTYPSD...YRVDQKVEYVCRLEEQM...NRF.VSERAP
S_cerevisiae	820	TLVSGISKSFGMCPAPETEMOYKKNFDEKISKVKECDANLVNLSNPEYKMYKLOP
A_thaliana	786	FSKSKKGDEVE.....KPKDSCSNKVSSVLOAKRAKEEHIPESPSRELC
C_elegans	725	IWLKTSNDSQHEQLLSCTEYV.....EDAGSSLCMTVARYRD...LSDAKTEKMEPL
M_musculus	839	ILTSHVKKTTPELE...IVLOKVQELQGNLPEDP...ESVSVEEALKYLLLVQVNELE
H_sapiens	839	ILTSHVKKTTPELE...IVLOKVHLEQGNAPSDF...DVSAAEALKYLLLVQVNELE
D_melanogaster	736	ITAVVVLGC...LE...MALQVKEQ...QE...DASLADLLOHLLLVQVNELE
S_cerevisiae	880	ITAVASQNFONLS...AALKLESELE.....NSEKKSCYTLCEPLQDVNVE
A_thaliana	831	ILTLASDPPATESLERKESVREMLLNSDDIRKKSQPSADEALKHLLWQDSEAF
C_elegans	777	ILTLALSKSPSKVNC...LKEVQE...HVERHADKDMFERNSSHHSFVPKAKELP
M_musculus	892	NHSLGTYDFNLVLMVAEKSQKDPKEYLPFLNLTKK.METNYORETIDKYLKRYEKALGHL
H_sapiens	892	DHSLGTYDFNLVLMVAEKSQKDPKEYLPFLNLTKK.METNYORETIDKYLKRYEKALGHL
D_melanogaster	782	NVALGTYDFGLVLFVAKSKQKDPKEYLPFLNLTKA.TPIDYRKFRIDDELKRYTSALSHL
S_cerevisiae	926	KSALSTYDVSLALVVAEKSQMDPKEYLPFLQELQD.NEPLRRKFLIDDLGNRYKALEHL
A_thaliana	891	EAALGLVDNLAAVVALNSQMDPKELPFLQELQK.MPESLMHKIDIKLQRTSALRNF
C_elegans	829	NCAALSTYDLKLAQQVAEASKYDPKEYLPVLNKNRVMCTLERQRIINVVREAWDAMSSL
M_musculus	951	.....SKCGPE..YFTECLNLIKDR.NLYKEATKLYRPDSPOYOAMSMAYGEHLMOEHE
H_sapiens	951	.....SKCGPE..YFTECLNLIKDR.NLYNEATKLYSPSSQOYODISIAYGEHLMOEHE
D_melanogaster	841	.....ACCGED..HMEALEYIEKH.GLYTBGLATYREHIEFQKNLYVAYABHRAIAK
S_cerevisiae	985	.....SEIDKSGNVSEEVYNYESH.DLYHSLALYRYDSEKQVLYNYIAKHSSNQY
A_thaliana	950	.....VSAG..VGYPDCNLIKNPFLPLGLLIT.DPERKLVYLSAWABHLEDER
C_elegans	889	FLDSSKERGSEETWNNIEHIOHEKLYQDALTIVKPGDRRKQCCCLYAAELERKVH
M_musculus	1002	YEPAGLVARCCGAQEKAEAFILACGSFOQALCVAAOLQMSKDKVAGLARTLAGKLVQORK
H_sapiens	1002	YEPAGLVARCCGAHEKALSALFLCCGFWQALCVAAOLNETKDOLHGLERTLAGKLVQORK
D_melanogaster	892	LDNASLMYERGGOLOQALSAKHTLQORVLEAKKLEPLDOV...AQSLVGLQVQOCH
S_cerevisiae	1038	YTDAAVAYEMLGKLEAMGAYOSAKRREAMSFAVOKEP.EEVESVAEELISSITFEH
A_thaliana	1001	VEDAATITLCCCKLEKASKARECGDWSGVLRVGCALKLGKDESKLAYELCEEKNALGK
C_elegans	948	WREAAFLYELSGNSEKTEKCEWMSRDVDGLAASARRBAVDAGKDKIBAIKMTTTRBARO

Figure 9

Continued

M_musculus	1062	HSEAAVLECYAQQYEEAVLLLEGSAWEEALRLVYKYDRVDIIETSEKPSILEAQRNYM
H_sapiens	1062	HSEAAVLECYAQQYEEAVLLLEGSAWEEALRLVYKYDRVDIIETSEKPSILEAQRNYM
D_melanogaster	949	HSEAYEYKSHCQQRKQFDLLEGHLYSRAYEAGLEDDVSEKAPLAYGVLE
S_cerevisiae	1096	YVBAADQLSYLDNVKEAVAYCKYRYNIAISLAIKAKHDEEVEVDEGGEGFGIA
A_thaliana	1061	PAEAAKHALYCSQISGSSSLNREFEALRYALHTADDRISVVKSSALECASCQ
C_elegans	1008	PKELAKAKKLAESSSTIVHLLCFEFLDASREVEVGK.....EPAKKKALSREDE
M_musculus	1122	DFLDSQTATFERHKNRLQVVRALRRQAPVHYDHEVAHGPESDLFSETSSIS.GSEMS
H_sapiens	1122	DFLDSQTATFERHKNRLQVVRALRRQAPVHYDHEVAHGPESDLFSETSSIS.GSEMS
D_melanogaster	1007	SSLQNLQLSEHYKQRLLDNRNOAKEGEEEDTEV.NLKEVDLLSDTSSHS..S.VS
S_cerevisiae	1156	ELADCKGQINSQRLRLREPAKKEENRYAFYGEETEQADEVSHAPSETSTQSFERYE
A_thaliana	1120	SEFKESIEKVGKYLTRYLAVERALLLAALKSEERSVVDLDDDTASESSNESGMSALF
C_elegans	1063	MDERRKTEGENYKRLAVVRENKLRVQFAAGEV.....DDLRDDISVSSISSR..
M_musculus	1180	.GKYSHSNR..ISARSSKNRR..KAERKKHSLKEGSPLEGLALLEAL....SEVVO.SVE
H_sapiens	1180	.GKYSHSNR..ISARSSKNRR..KAERKKHSLKEGSPLEGLALLEAL....SEVVO.SVE
D_melanogaster	1063	.GTSRATCK...FRSSKNRR..KHERKLFSLKPCNPEDFALDADHNVKKAQ..Q
S_cerevisiae	1216	.GKTGGAKKKGASRTAKNRK..KZERKARGKMGNIYEE...EVLVQSVGRTSE.RLN
A_thaliana	1180	LGTRGSAKSVSSSNATSRADLRORNSGKELAGSAGEALVDEH.....KCHR.MDE
C_elegans	1115	.....SGSKYSMASTVRRKK.QIERKSSSLKEGGEYEDSALLNVLSENYRWENIGSE
M_musculus	1231	KLKDEVHAILKVLFLFEFDEQKELQRAFEESTLQLMERAUPEIWTBAGQOSS..ATPVLC
H_sapiens	1231	KLKDEVHAILKVLFLFEFDEQKELQRAFEESTLQLMERAUPEIWTBAGQOSS..ATPVLC
D_melanogaster	1116	PVRDTCKAHLQANAAADPLAALQREKTLQAYDAADDEIWTPELRGNGLEAHTTG
S_cerevisiae	1268	QTKPDVAVRVEGLCRNMREQAHSEKNEVYVDLTKANVKEIYSISEKDRERVNEN..G
A_thaliana	1234	GGKRELKSHICLVTLGEMESAOKLOQTAEN.FOYSQVAVEL.AHDTVSSSEVDEEVC
C_elegans	1168	FCFPWFNFI.....
M_musculus	1289	PSSTANSIMASYQQQKTCVPALDAGVPPKMDPRSQWKLSLLE
H_sapiens	1289	PNSTANSIMASYQQQKTSVPFLDAEFPKPKINRSTOWKLSLLD
D_melanogaster	1176	PN..VDYFALQKEQRYNLSPDKR..GKQLI..MMDWQHETLQ
S_cerevisiae	1326	EVYIPEIPVPEIHDFPKSHSYDF.....
A_thaliana	1292	PERYQKTRSTWARDSDTFSWKK..VFISE.....
C_elegans	1178	.....

Figure 9  
Continued

TABLE 2. COMPARISON OF THE NOVEL MOUSE *Ikbkap* GENE WITH MULTIPLE SPECIES HOMOLOGS

Species	Gene name	No. of amino acids	Molecular weight (kDa)	% aa identity with M.m.	GenBank Accession No.
<i>Mus musculus</i> (M.m.)	<i>Ikbkap</i>	1332	149.11	—	AF367244
<i>Homo sapiens</i>	<i>IKBKAP</i>	1332	149.11	80	AF153419
<i>Drosophila melanogaster</i>	<i>CG10535</i>	1213	138.21	32	AAF54670
<i>Saccharomyces cerevisiae</i>	<i>Elp1/Iki3p</i>	1349	152.99	29	AAB67278
<i>Arabidopsis thaliana</i>	Unknown	1308	146.63	27	BAB08695
<i>Caenorhabditis elegans</i>	Unknown	1177	134.80	24	AAF60430

Figure 10

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TABLE 1. MOUSE *Ikbkap* EXON AND INTRON BOUNDARIES

Exon	Acceptor site	Donor site	Size (bp)	cDNA position
1		AGgtgagcattcgcccg	129	1..129 <sup>a</sup>
2	ttttttccctcagAA	AAgtaggctcactgatgc	163	130..292 <sup>b</sup>
3	tatgctttgtgaaagGT	AGgtagggtgaaggcct	153	293..445
4	ttttctctgatgcagCT	AGgtaagctttgcactg*	82	446..527
5	acatgaactcctaagCT	AGgtaagcggtttctgg	81	528..608
6	cttgaaaaactgtagGC	TGgtaagcggggatgat	86	609..694
7	gggtctctcttcagCC	TGgtgtctctcttcagc*	97	695..791
8	ctacctcctttgcagAG	AAgtgagtggacataaa*	91	792..882
9	agggtctgcttcagAC	AGgtagggtcagagtt	124	883..1006
10	ttttgtccctaccagGT	TGgtatgacagcttg	94	1007..1100
11	tcctccacacacagTC	AAgtaagttgctgcgaa	231	1101..1331
12	ctttcatgtgtagAC	TGgtgaagtggaagcagg	165	1332..1496
13	tttttgtttctagGT	TCgtaagttcctaata	100	1497..1596
14	ctaataattgaacagGA	AGgtatcatgtgtcatc	189	1597..1785
15	ttttttgctttagTT	GGgtgaggatcagagtt	107	1786..1892
16	ttaatcttacaacagAG	AGgtgaatgacacggc	104	1893..1996
17	ttcatttcttgacagGA	AGgtatgtaggcttgg	54	1997..2050
18	tcttgccgttgacagGT	AAgtaagctctctata	106	2051..2156
19	cactggtatttttagTG	AGgtaagctgactcttc*	116	2157..2272
20	gggttttttttagAT	AAgtaagtatttattct*	74	2273..2346
21	ttcctgtcctcacagAC	AGgtacactttgcgtct	79	2347..2425
22	tactttcttgatagGT	AGgtatgtatttgata*	80	2426..2505
23	tactgtggttcttagGG	AAgtgggtgctgtgtgt	138	2506..2643
24	cacttactacctcagGT	AGgtagagacctgcgcg*	86	2644..2729
25	cttaaaactccaacagGA	AGgtatgtggagttgag*	149	2730..2878
26	aacttttttctaggGA	TGgtaagggttttttt	124	2879..3002
27	ttttttttttcagGA	AGgtatgtgggtgggta*	98	3003..3100
28	cgtctctgtcacagGC	AGgtaagcagggccatt	202	3101..3302
29	ttgctgtcttttcagGA	AGgtgagctcctcccg	62	3303..3364
30	ctcttccctgtcagGA	TGgtaaggagctctga	63	3365..3427
31	tttcttccctcttagGT	AGgtgaggattacatt*	61	3428..3488
32	attatgcacctcagCC	GGgtgagtgctccaaa*	114	3489..3602
33	gttcattctcttagAT	GCgtacgtacgagacct*	112	3603..3714
34	tgtaatttctgacagGA	AGgtatggcttcagtgc	128	3715..3842
35	ccattttctcttagAT	CGgtaagcttccctcaga	155	3843..3997
36	ctgtttctgcttagGT	CGgtgtactgtctgttc	76	3998..4073
37	cattcttgcttcagAT		709	4074..4799 <sup>c</sup>

Figure 11

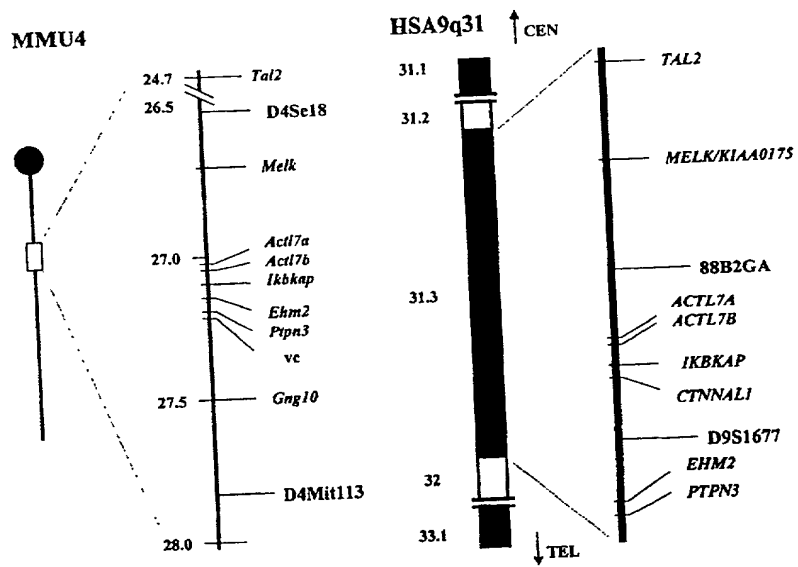


Figure 12

1004.1355 - 0.10702